SEQUENCE LISTING

SEQ ID NO: 1
SEQUENCE TYPE: Amino acid
SEQUENCE LENGTH: 9
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
SEQUENCE
Xxx Glu Thr Ile Asn Xxx His Phe Lys
1 5 9

SEQ ID NO: 2
SEQUENCE TYPE: Amino acid
SEQUENCE LENGTH: 7
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
SEQUENCE
Xxx Gln Xxx Ala Phe Thr Lys
1 5 7

SEQ ID NO: 3
SEQUENCE TYPE: Amino acid
SEQUENCE LENGTH: 19
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
SEQUENCE
Val Glu Xxx Val Asp Phe Thr Asn His Leu Glu Asp Thr Xxx Xxx Asn
1 5 10 15
Ile Asn Lys
19

SEQ ID NO: 4
SEQUENCE TYPE: Amino acid
SEQUENCE LENGTH: 17
TOPOLOGY: Linear

MOLECULE TYPE: Peptide

SEQUENCE

Xxx Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala Xxx Ala

1 5 10 15

Ala Xxx Gly

17

SEQ ID NO: 5

SEQUENCE TYPE: Amino acid

SEQUENCE LENGTH: 9

TOPOLOGY: Linear

MOLECULE TYPE: Peptide

SEQUENCE

Xxx Tyr Leu Arg Ala Leu Gly Leu Lys

1 5 9

SEQ ID NO: 6

SEQUENCE TYPE: Amino acid

SEQUENCE LENGTH: 20

TOPOLOGY: Linear

MOLECULE TYPE: Peptide

SEQUENCE

Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg

1 5 10 15

Met Xxx Gly Lys

20

SEQ ID NO: 7

SEQUENCE TYPE: Amino acid

SEQUENCE LENGTH: 5

TOPOLOGY: Linear

MOLECULE TYPE: Peptide

SEQUENCE

Leu Tyr Asp Ala Lys

1 5

SEQ ID NO: 8
SEQUENCE TYPE: Amino acid
SEQUENCE LENGTH: 5
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
SEQUENCE
Asn Tyr Glu Met Lys
1 5

SEQ ID NO: 9
SEQUENCE TYPE: Amino acid
SEQUENCE LENGTH: 10
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
SEQUENCE
Ala Val Ala Met Met His Gln Xxx Arg Lys
1 5 10

SEQ ID NO: 10
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 38
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
FEATURES: corresponding to amino acid sequence of SEQ ID NO: 3; I is inosine.
SEQUENCE
GTIGARIIIG TIGAYTTYAC IAAYCAYYTI GARGAYAC 38

SEQ ID NO: 11
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 32
STRANDNESS: Single
TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA
FEATURES: corresponding to amino acid sequence of SEQ ID NO: 4; I is inosine.
SEQUENCE
TACATCGAIG TIACIGARGA RGGIACNGAR GC 32

SEQ ID NO: 12
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 37
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
FEATURES: Oligomer attached to 3'-RACE kit (Gibco BRL).
SEQUENCE
GGCCACGCGT CGACTAGTAC TTTTTTTTTT TTTTTTT 34

SEQ ID NO: 13
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 20
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
ATGTTGTGGG GACTGCTATA 20

SEQ ID NO: 14
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 23
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
CAAGGCGAAT GACCTCTAAG TAT 23

SEQ ID NO: 15
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 21
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
CCCCGAAGCA ATCCCAGAGA G 21

SEQ ID NO: 16
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 21
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
CTCAGGCAGC AGAACGTACA T 21

SEQ ID NO: 17
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 21
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
GGCGACGACT CCTGGAGCCC G 21

SEQ ID NO: 18
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 22
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
GACACCAGAC CAACTGGTAA TG 22

SEQ ID NO: 19
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 36
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
CATCCGGGAG ATGTACAGCC GGCCGCCAGA GGCAAT 36

SEQ ID NO: 20
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 21
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
GCTGTGGCCA TGATGCACCA G 21

SEQ ID NO: 21
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 24
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
TACCTGCGGG CCCTGGGCCT GAAG 24

SEQ ID NO: 22
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 51
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE

CATCCGGGAG ATGTACAGCC GGCCGCCAGA GGCAATGCCA GACAGGTCAG C 51

SEQ ID NO: 23
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 17
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
GTTTTCCCAG TCACGAC 17

SEQ ID NO: 24
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 17
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
CAGGAAACAG CTATGAC 17

SEQ ID NO: 25
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 20
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
AATTATGGCC CACACCAGTG 20

SEQ ID NO: 26
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 20
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA

SEQUENCE
ACTAGCCGCT ACAGTCAACA 20

SEQ ID NO: 27
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 21
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
TTGCCACTTG CCTTTGAAGT A 21

SEQ ID NO: 28
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 21
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
CTGATGCATC ATGGCGACTG C 21

SEQ ID NO: 29
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 21
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
AGCATTCACC AGCACCATTA C 21

SEQUENCE ID NO: 30
SEQUCNE TYPE: Nucleic acid
SEQUENCE LENGTH: 1950
STRANDNESS: Double
TOPOLOGY: Linear

MOLECULE TYPE: complimentary DNA (cDNA)
ORIGINAL SOURCE: Human
IMMEDIATE SOURCE: A431
FEATURE: DNA coding for human megakaryocyte differentiation factor
SEQUENCE

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GGCACGAGAG GAACTGAAGC CCAGCTGTGA AGGCCGCAGA CTGCAGTGAG          50
AGGAGGCTGC ACTCCATTTT GCA ATG GCC TCC CTT GCT GCA GCA AAT      97
                          Met Ala Ser Leu Ala Ala Ala Asn
                            1               5
GCA GAG TTT TGC TTC AAC CTG TTC AGA GAG ATG GAT GAC AAT CAA  142
Ala Glu Phe Cys Phe Asn Leu Phe Arg Glu Met Asp Asp Asn Gln
     10                  15                  20
GGA AAT GGA AAT GTG TTC TTT TCC TCT CTG AGC CTC TTC GCT GCC  187
Gly Asn Gly Asn Val Phe Phe Ser Ser Leu Ser Leu Phe Ala Ala
     25                  30                  35
CTG GCC CTG GTC CGC TTG GGC GCT CAA GAT GAC TCC CTC TCT CAG  232
Leu Ala Leu Val Arg Leu Gly Ala Gln Asp Asp Ser Leu Ser Gln
     40                  45                  50
ATT GAT AAG TTG CTT CAT GTT AAC ACT GCC TCA GGA TAT GGA AAC  277
Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser Gly Tyr Gly Asn
     55                  60                  65
TCT TCT AAT AGT CAG TCA GGG CTC CAG TCT CAA CTG AAA AGA GTT  322
Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu Lys Arg Val
     70                  75                  80
TTT TCT GAT ATA AAT GCA TCC CAC AAG GAT TAT GAT CTC AGC ATT  367
Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu Ser Ile
     85                  90                  95
GTG AAT GGG CTT TTT GCT GAA AAA GTG TAT GGC TTT CAT AAG GAC  412
Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys Asp
    100                 105                 110
TAC ATT GAG TGT GCC GAA AAA TTA TAC GAT GCC AAA GTG GAG CGA  457
Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg
    115                 120                 125
GTT GAC TTT ACG AAT CAT TTA GAA GAC ACT AGA CGT AAT ATT AAT  502
Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn
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    130                 135                 140
AAG TGG GTT GAA AAT GAA ACA CAT GGC AAA ATC AAG AAC GTG ATT  547
Lys Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile
    145                 150                 155
GGT GAA GGT GGC ATA AGC TCA TCT GCT GTA ATG GTG CTG GTG AAT  592
Gly Glu Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn
    160                 165                 170
GCT GTG TAC TTC AAA GGC AAG TGG CAA TCA GCC TTC ACC AAG AGC  637
Ala Val Tyr Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser
    175                 180                 185
GAA ACC ATA AAT TGC CAT TTC AAA TCT CCC AAG TGC TCT GGG AAG  682
Glu Thr Ile Asn Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys
    190                 195                 200
GCA GTC GCC ATG ATG CAT CAG GAA CGG AAG TTC AAT TTG TCT GTT  727
Ala Val Ala Met Met His Gln Glu Arg Lys Phe Asn Leu Ser Val
    205                 210                 215
ATT GAG GAC CCA TCA ATG AAG ATT CTT GAG CTC AGA TAC AAT GGT  772 Ile Glu
Asp Pro Ser Met Lys Ile Leu Glu Leu Arg Tyr Asn Gly
    220                 225                 230
GGC ATA AAC ATG TAC GTT CTG CTG CCT GAG AAT GAC CTC TCT GAA  817
Gly Ile Asn Met Tyr Val Leu Leu Pro Glu Asn Asp Leu Ser Glu
    235                 240                 245
ATT GAA AAC AAA CTG ACC TTT CAG AAT CTA ATG GAA TGG ACC AAT  862
Ile Glu Asn Lys Leu Thr Phe Gln Asn Leu Met Glu Trp Thr Asn
    250                 255                 260
CCA AGG CGA ATG ACC TCT AAG TAT GTT GAG GTA TTT TTT CCT CAG  907
Pro Arg Arg Met Thr Ser Lys Tyr Val Glu Val Phe Phe Pro Gln
    265                 270                 275
TTC AAG ATA GAG AAG AAT TAT GAA ATG AAA CAA TAT TTG AGA GCC  952
Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys Gln Tyr Leu Arg Ala
    280                 285                 290
CTA GGG CTG AAA GAT ATC TTT GAT GAA TCC AAA GCA GAT CTC TCT  997
Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys Ala Asp Leu Ser
    295                 300                 305
GGG ATT GCT TCG GGG GGT CGT CTG TAT ATA TCA AGG ATG ATG CAC 1042
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Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg Met Met His
    310                 315                 320
AAA TCT TAC ATA GAG GTC ACT GAG GAG GGC ACC GAG GCT ACT GCT 1087
Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala Thr Ala
    325                 330                 335
GCC ACA GGA AGT AAT ATT GTA GAA AAG CAA CTC CCT CAG TCC ACG 1132
Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr
    340                 345                 350
CTG TTT AGA GCT GAC CAC CCA TTC CTA TTT GTT ATC AGG AAG GAT 1177
Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp
    355                 360                 365
GAC ATC ATC TTA TTC AGT GGC AAA GTT TCT TGC CCT TGA         1216
Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro ...
    370                 375                 380
AAATCCAATT GGTTTCTGTT ATAGCAGTCC CCACAACATC AAAGAACCAC      1266
CACAAGTCAA TAGATTTGAG TTTAATTGGA AAAATGTGGT GTTTCCTTTG      1316
AGTTTATTTC TTCCTAACAT TGGTCAGCAG ATGACACTGG TGACTTGACC      1366
CTTCCTAGAC ACCTGGTTGA TTGTCCTGAT CCCTGCTCTT AGCATTCTAC      1416
CACCATGTGT CTCACCCATT TCTAATTTCA TTGTCTTTCT TCCCACGCTC      1466
ATTTCTATCA TTCTCCCCCA TGACCCGTCT GGAAATTATG GAGAGTGCTC      1516
AACTGGTAAG GAGAACGTAG AAGTAGCCCT AGGGATCCTT TTTGAAACTC      1566
TACAGTTATC GCAGATATTC TAGCTTCATT GTAAGCAATC TAGGAAATAA      1616
GCCCTGCTGC TTTCTAGAAA TAAGTGTGAA GGATAAATTT TCTTTGTTGA      1666
CCTATGAAGA TTTTAGAGTT TACCTTCATA TGTTTGATTT TAAATCAGTG      1716
TATAATCTAG ATGGTAAAAA ATGTGAAATT GGGATTAGGG ACCAACCAAA      1766
ATATTTCATT AATGCTTTCA ATTGACAAAT TTTGGTCTTT CTTTGATAAG      1816
ACAATATGTA CATAGTTTTT TCAAATATTA AAGATCTTTT AACTGTTGGC      1866
AGTTGTTATC TACAGAATCA TATCTCATAT GCTGTGTAGT TTATAAGTTT      1916
TTTCTCTATT TATCAGAATA AAGAAATACA ACAT                       1950
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SEQ ID NO: 31

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 20

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA
ORIGINAL SOURCE: Human
FEATURES: 5'-non-translation region
SEQUENCE
AACTGAAGCC CAGCTGTGAA 20

SEQ ID NO: 32
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 37
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
CTCGAATTCG CGATGGCCTC CCTTGCTGCA GCAAATG 37

SEQ ID NO: 33
SEQUENCE TYPE: Nucleic acid
SEQUENCE LENGTH: 49
STRANDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
SEQUENCE
GGGAATTCGC GGCCGCGTGG TGGTTCTTTG ATGTTGTGGG GACTGCTAT 49